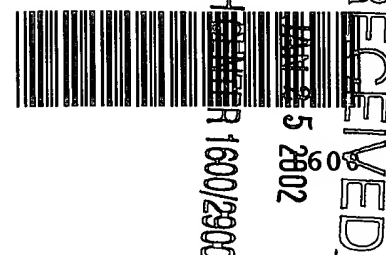


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 PATENT APPLICATION: US/09/927,315

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3 <110> APPLICANT: Zuker, Charles S.
 4 Ryba, Nicholas J.P.
 5 Nelson, Greg
 6 Hoon, Mark A.
 7 Chandrashekar, Jayaram
 8 Zhang, Yifeng
 9 The Regents of the University of California
 10 The Government of the United States of America
 11 as represented by the Secretary of the
 12 Department of Health and Human Services
 14 <120> TITLE OF INVENTION: Mammalian Sweet Taste Receptors
 16 <130> FILE REFERENCE: 02307E-120110US
 18 <140> CURRENT APPLICATION NUMBER: US 09/927,315
 19 <141> CURRENT FILING DATE: 2001-08-10
 21 <150> PRIOR APPLICATION NUMBER: US 60/302,898
 22 <151> PRIOR FILING DATE: 2001-07-03
 24 <160> NUMBER OF SEQ ID NOS: 25
 26 <170> SOFTWARE: PatentIn Ver. 2.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 840
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Rattus sp.
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: rat T1r1 sweet taste receptor
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 40 Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
 41 20 25 30
 43 Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
 44 35 40 45
 46 Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
 47 50 55 60
 49 Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
 50 65 70 75 80
 52 Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
 53 85 90 95
 55 Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
 56 100 105 110
 58 Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
 59 115 120 125
 61 Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
 62 130 135 140

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PATENT APPLICATION: US/09/927,315

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65 145 150 155 160
67 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
68 165 170 175
70 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
71 180 185 190
73 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
74 195 200 205
76 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
77 210 215 220
79 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
80 225 230 235 240
82 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
83 245 250 255
85 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
86 260 265 270
88 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
89 275 280 285
91 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
92 290 295 300
94 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
95 305 310 315 320
97 Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
98 325 330 335
100 Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
101 340 345 350
103 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
104 355 360 365
106 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
107 370 375 380
109 Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
110 385 390 395 400
112 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
113 405 410 415
115 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
116 420 425 430
118 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
119 435 440 445
121 Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
122 450 455 460
124 Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
125 465 470 475 480
127 Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
128 485 490 495
130 Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
131 500 505 510
133 His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
134 515 520 525
136 Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala

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Output Set: N:\CRF3\01162002\I927315.raw

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137      530      535      540
139 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
140 545      550      555      560
142 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
143      565      570      575
145 Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
146      580      585      590
148 Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
149      595      600      605
151 Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
152      610      615      620
154 Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
155 625      630      635      640
157 Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
158      645      650      655
160 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
161      660      665      670
163 Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
164      675      680      685
166 His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
167      690      695      700
169 Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
170 705      710      715      720
172 Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
173      725      730      735
175 Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
176      740      745      750
178 Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
179      755      760      765
181 Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
182      770      775      780
184 Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
185 785      790      795      800
187 Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
188      805      810      815
190 Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
191      820      825      830
193 Tyr Thr Arg Arg Cys Gly Thr Thr
194      835      840
197 <210> SEQ ID NO: 2
198 <211> LENGTH: 842
199 <212> TYPE: PRT
200 <213> ORGANISM: Mus musculus
202 <220> FEATURE:
203 <223> OTHER INFORMATION: mouse T1R1 sweet taste receptor
205 <400> SEQUENCE: 2
206 Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val
207 1 5 10 15
209 Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly

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Input Set : A:\Uc1201-1.app

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210		20		25		30	
212	Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His						
213		35		40		45	
215	Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp						
216		50		55		60	
218	Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met						
219	65		70		75		80
221	Arg Phe Thr Val Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn						
222		85		90		95	
224	Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn						
225		100		105		110	
227	Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu						
228		115		120		125	
230	Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu						
231		130		135		140	
233	Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu						
234	145		150		155		160
236	Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile						
237		165		170		175	
239	Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser						
240		180		185		190	
242	Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly						
243		195		200		205	
245	Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu						
246		210		215		220	
248	Gly Val Gln Ala Leu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val						
249	225		230		235		240
251	Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg						
252		245		250		255	
254	Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val						
255		260		265		270	
257	Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val						
258		275		280		285	
260	Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp						
261		290		295		300	
263	Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly						
264	305		310		315		320
266	Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys						
267		325		330		335	
269	Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr						
270		340		345		350	
272	Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys						
273		355		360		365	
275	His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met						
276		370		375		380	
278	Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly						
279	385		390		395		400
281	Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro						
282		405		410		415	

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285           420           425           430
287 Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
288           435           440           445
290 Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
291           450           455           460
293 Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
294 465           470           475           480
296 Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
297           485           490           495
299 Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
300           500           505           510
302 Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe
303           515           520           525
305 Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu
306           530           535           540
308 Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe
309 545           550           555           560
311 Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr
312           565           570           575
314 Leu Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg
315           580           585           590
317 Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu
318           595           600           605
320 Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe
321           610           615           620
323 Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser
324 625           630           635           640
326 Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln
327           645           650           655
329 Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
330           660           665           670
332 Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser
333           675           680           685
335 Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro
336           690           695           700
338 Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu
339 705           710           715           720
341 Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn
342           725           730           735
344 Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu
345           740           745           750
347 Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu
348           755           760           765
350 Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr
351           770           775           780
353 Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr
354 785           790           795           800
356 Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile

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VERIFICATION SUMMARY

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